

REMARKS/ARGUMENTS

Claims 20 and its dependent claims have been amended to avoid the 35 U.S.C. 112, second paragraph, objection. Thus, except for attending to the 35 U.S.C. 112 objections noted by the Board in its "Vacatur and Remand to the Examiner" and the relatively minor 35 U.S.C. 112, second paragraph, objections noted by the Examiner, claim 20 and its dependent claims have been returned to essentially the same form as they were before the Board.

The Examiner rejected claim 26 under 35 U.S.C. 102(b) as being anticipated by Fleischmann et al (Whole-Genome Random Sequencing and Assembly of Haemophilus Influenzae Rd. Science Vol. 269, pages 496-498, 1-12) (hereinafter Fleischmann), and this ground of rejection is respectfully traversed. Claim 26 is directed to a method of

...detecting connectron control [C1, C2] and targets [T1, T2] sequences in a given genome comprising:
by computer ... determining one or more sites of control [C1, C2] sequence organization, and/or
determining one or more sites of target [T1, T2] application and outputting the results thereof to a utilization facility.

Fleishmann has nothing to do with connectrons but is directed to whole genome random sequencing and assembly of Haemophilus influenzae Rd. Nothing is said about determining one or more sites of control sequence or target application.

The Examiner seeks to avoid the Board's vacatur remand and amplified in some respects his grounds and reasoning under 35

U.S.C. 112, first paragraph, to wit, the Examiner now contends that all claims:

...are drawn to analysis of connectrons and connectron analysis cannot be used by one of skill in the art.... The Board stated that the claimed subject matter only appeared to require locating connectrons in sequence data, however the rejection for lack of enablement acknowledges that locating connectrons in sequence data can be performed but that the result of the analysis cannot be used by one of skill in the art. (Paragraph 2 on page 2 of the Office Action.)

The rejection of claims 20-37 under 35 U.S.C. 112, first paragraph, is respectfully traversed. The Examiner again cites *In re Wands* (8 USPQ 2d 1400 (CAFC 1988) and contends that there would be "an unpredictable amount of experimentation required to practice the claimed invention." Then on page 6 beginning in paragraph b) extending to the first paragraph of page 9, the Examiner goes into a series of commentary regarding what is not in the specification such as:

The specification speculates without evidence on pages 1-3 that triple-stranded (triplex) structures will form between RNA and double stranded DNA in chromatin where connectron symmetries are identified. The specification does not provide guidance that there are any limitations on formation of triplex structures, and only implies that regions of RNA with identical sequence to one strand of a double stranded DNA sequence will form triplex structures.... (Page 6, first full paragraph.)

The Examiner goes to a number of issues that are allegedly not discussed in the specification. None of them, however, relate to what is claimed. In the words of the Board in its vacatur:

The specification states that an algorithm has been developed "to determine the connectron structure of any genome," id. at 2. and Figure 8 provides an overall view of the algorithm. see id. at 28. As can be seen in

Figure 8, the algorithm analyzes a genome for possible connectrons. Moreover, according to the specification, the physical experimentation process of proving the existence and lifetimes of connectrons "is logically quite separate from the computational experimentation that have been conducted from June or 1999 to May of 2001," id. at 28, which has demonstrated the existence of connectrons in prokaryotes, plants,, higher animals and humans using publicly available genomes, see id. at 35, 37 and 38.

Claim 20, which is only one of the eight independent claims, is drawn to:

A computer mediated method of identifying DNA sequences that control the expression of different collections of genes in a genome comprising detecting, by computer, one or more pairs of first and second non-adjacent DNA sequences which could bind to one RNA molecule such that a first RNA sequence in that RNA molecule can bind a first non-adjacent DNA sequence and a second RNA sequence in that RNA molecule can bind to a second non-adjacent sequence.

The rejection is set forth on pages 3-5 of the Examiner's Answer, but it suffers from several deficiencies.

First, there are eight independent claims, each having different limitations. For example, claim 21 requires "detecting, by computer, changes in connectron behavior in the genome as a function of changes in the sequence of the genome." The rejection, however, does not address the limitations of all of the independent claims, nor does it address the limitations of dependent claims 37.

Second, the rejection appears to address limitations that do not seem to appear in the claims. The examiner focuses on the issue that "[i]n order to practice the claimed invention one of skill in the art must identify and use a connectron to predict regulation of gene expression." Examiner's Answer, page 3. Claim 20, for example does not require predicting regulation of gene expression, but only appears to require locating possible connectrons.

Clearly, the Examiner appears to recognize the import of this portion of the Board's decision. Applicant does not require the allegedly missing material.

At any rate, the two declarations (James V. Oberthaler and Richard W. Pastor) largely rebut the Examiner's contention.

In view of the above, further and favorable reconsideration is respectfully requested.

Respectfully submitted,

A handwritten signature in black ink, appearing to read "Jim Zegeer".

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In the event this paper is deemed not timely filed, the applicant hereby petitions for an appropriate extension of time. The fee for this extension may be charged to Deposit Account No. 26-0090 along with any other additional fees which may be required with respect to this paper